

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/500,207
Source: PT/10
Date Processed by STIC: 7/8/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

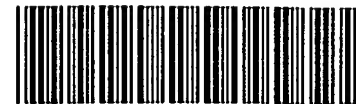
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby Room 1B03, Arlington, VA 22202

Revised 05/17/04

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: <u>10/500,207</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <input checked="" type="checkbox"/> Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 <input checked="" type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
10 <input type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 <input type="checkbox"/> Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input type="checkbox"/> Misuse of n/Xaa	"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid	



PCT

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/500,207

DATE: 07/08/2004

TIME: 16:15:05

Input Set : A:\Seq. Listing.asc

Output Set: N:\CRF4\07082004\J500207.raw

3 <110> APPLICANT: KYOWA HAKKO KOGYO CO., LTD
 5 <120> TITLE OF INVENTION: AGENT FOR TREATING ARTHRITIS
 7 <130> FILE REFERENCE: 1442
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/500,207
 C--> 9 <141> CURRENT FILING DATE: 2004-06-28
 9 <150> PRIOR APPLICATION NUMBER: JP2001-400677
 10 <151> PRIOR FILING DATE: 2001-12-28
 12 <160> NUMBER OF SEQ ID NOS: 51
 14 <170> SOFTWARE: PatentIn version 3.1

IMPORTANT: see
item 4 on

Error Summary
 Sheet. Saved
 file must have a
 .txt extension
 (text)

ERRORED SEQUENCES

16 <210> SEQ ID NO: 1
 17 <211> LENGTH: 420
 18 <212> TYPE: DNA
 19 <213> ORGANISM: Mus musculus
 21 <220> FEATURE:
 22 <223> OTHER INFORMATION: Inventor: Tamura, Tadafumi; Uchii, Masako; Toshio,
 23 Suda
 24 Inventor: Ichiro, Miki; Akira, Tanaka
 26 <220> FEATURE:
 27 <221> NAME/KEY: source
 28 <222> LOCATION: (1)..(420)
 29 <223> OTHER INFORMATION: /organism="Mus musculus"
 31 <220> FEATURE:
 32 <221> NAME/KEY: CDS
 33 <222> LOCATION: (1)..(420)
 35 <220> FEATURE:
 36 <221> NAME/KEY: sig_peptide
 37 <222> LOCATION: (1)..(57)
 39 <400> SEQUENCE: 1
 E--> 40 atg gaa tgg atc tgg atc ttt ctc ttc ttc ctc tca gga act aca
 41 ggt 48
 42 Met Glu Trp Ile Trp Ile Phe Leu Phe Phe Leu Ser Gly Thr Thr
 W--> 43 Gly
 W--> 44 1 5 10 15
 E--> 46 gtc tac tcc cag gtt cag ctg cag cag tct gga gct gag gtg gcg
 47 agg 96
 48 Val Tyr Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Val Ala
 W--> 49 Arg
 W--> 50 20 25 30
 E--> 52 ccc ggg gct tca gtg aaa ctg tcc tgc aag gct tct ggc tac acc

Does Not Comply
 Corrected Diskette Needed
 see pp 1-22

move inventors to <110> line
 They belong on
 <110> APPLICANT: line

global
 format error
 (see item 1 on
 Error Summary
 Sheet)

RAW SEQUENCE LISTING

DATE: 07/08/2004

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Input Set : A:\Seq. Listing.asc

Output Set: N:\CRF4\07082004\J500207.raw

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53 ttc      144
54 Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr
W--> 55 Phe
W--> 56      35      40      45
E--> 58 act gac tac tat cta aac tgg gtg aag cag agg tct gga cag ggc
59 ctt      192
60 Thr Asp Tyr Tyr Leu Asn Trp Val Lys Gln Arg Ser Gly Gln Gly
W--> 61 Leu
W--> 62      50      55      60
E--> 64 gag tgg att gga gag att gat cct gga agt gat agt ata tat tat
65 aat      240
66 Glu Trp Ile Gly Glu Ile Asp Pro Gly Ser Asp Ser Ile Tyr Tyr
W--> 67 Asn
W--> 68      65      70      75
E--> 69 80
E--> 71 gaa aac ttg gag ggc agg gcc aca ctg act gca gac aaa tcc tcc
72 agc      288
73 Glu Asn Leu Glu Gly Arg Ala Thr Leu Thr Ala Asp Lys Ser Ser
W--> 74 Ser
W--> 75      85      90      95
E--> 77 aca gcc tac atg cag ctc aac agc ctg aca tct gag gac tct gca
78 gtc      336
79 Thr Ala Tyr Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala
W--> 80 Val
W--> 81      100      105      110
E--> 83 tat ttc tgt gca aga tat ggg tat tct aga tac gac gta agg ttt
84 gtc      384
85 Tyr Phe Cys Ala Arg Tyr Gly Tyr Ser Arg Tyr Asp Val Arg Phe
W--> 86 Val
W--> 87      115      120      125
E--> 89 tac tgg ggc caa ggg act ctg gtc act gtc tct aca
90 420
91 Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Thr
W--> 92      130      135      140
95 <210> SEQ ID NO: 2
96 <211> LENGTH: 140
97 <212> TYPE: PRT
98 <213> ORGANISM: Mus musculus
100 <220> FEATURE:
101 <221> NAME/KEY: SIGNAL
102 <222> LOCATION: (1)..(19)
104 <400> SEQUENCE: 2
105 Met Glu Trp Ile Trp Ile Phe Leu Phe Phe Leu Ser Gly Thr Thr
E--> 106 Gly
E--> 107 1      5      10      15
110 Val Tyr Ser Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Val Ala
E--> 111 Arg
E--> 112      20      25      30
115 Pro Gly Ala Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr

```

same error

same

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```

E--> 116 Phe
E--> 117          35          40          45
      120 Thr Asp Tyr Tyr Leu Asn Trp Val Lys Gln Arg Ser Gly Gln Gly
E--> 121 Leu
E--> 122          50          55          60
      125 Glu Trp Ile Gly Glu Ile Asp Pro Gly Ser Asp Ser Ile Tyr Tyr
E--> 126 Asn
E--> 127          65          70          75
E--> 128 80
      131 Glu Asn Leu Glu Gly Arg Ala Thr Leu Thr Ala Asp Lys Ser Ser
E--> 132 Ser
E--> 133          85          90          95
      136 Thr Ala Tyr Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala
E--> 137 Val
E--> 138          100          105          110
      141 Tyr Phe Cys Ala Arg Tyr Gly Tyr Ser Arg Tyr Asp Val Arg Phe
E--> 142 Val
E--> 143          115          120          125
      146 Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Thr
E--> 147          130          135          140
      150 <210> SEQ ID NO: 3
      151 <211> LENGTH: 393
      152 <212> TYPE: DNA
      153 <213> ORGANISM: Mus musculus
      155 <220> FEATURE:
      156 <221> NAME/KEY: source
      157 <222> LOCATION: (1)..(393)
      158 <223> OTHER INFORMATION: /organism="Mus musculus"
      160 <220> FEATURE:
      161 <221> NAME/KEY: CDS
      162 <222> LOCATION: (1)..(393)
      164 <220> FEATURE:
W--> 165 <221> NAME/KEY: signal_peptide
      166 <222> LOCATION: (1)..(57)
      168 <400> SEQUENCE: 3
E--> 169 atg aag ttg cct gtt agg ctg ttg gtg ctg atg ttc tgg att cct
      170 gct          48
      171 Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro
W--> 172 Ala
W--> 173          1          5          10          15
E--> 175 tcc agg agt gat gtt ttg atg acc caa act cca ctc tcc ctg cct
      176 gtc          96
      177 Ser Arg Ser Asp Val Leu Met Thr Gln Thr Pro Leu Ser Leu Pro
W--> 178 Val
W--> 179          20          25          30
E--> 181 agt ctt gga gat caa gcc tcc atc tct tgc aga tct agt cag agt
      182 ctt          144
      183 Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser
W--> 184 Leu

```

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```

W--> 185          35          40          45
E--> 187 gta cat agt aat gga aga acc tat tta gaa tgg tac ctg cag aaa
      188 cct          192
      189 Val His Ser Asn Gly Arg Thr Tyr Leu Glu Trp Tyr Leu Gln Lys
W--> 190 Pro
W--> 191          50          55          60
E--> 193 ggc cag tca cca aag gtc ctg atc tac aaa gtt tcc aac cga att
      194 tct          240
      195 Gly Gln Ser Pro Lys Val Leu Ile Tyr Lys Val Ser Asn Arg Ile
W--> 196 Ser
W--> 197          65          70          75
E--> 198 80
E--> 200 ggg gtc cca gac agg ttc agt ggc agt gga tca ggg aca gat ttc
      201 aca          288
      202 Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
W--> 203 Thr
W--> 204          85          90          95
E--> 206 ctc aaa atc agc aga gtg gag gct gag gat ctg gga gtt tat ttc
      207 tgc          336
      208 Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe
W--> 209 Cys
W--> 210          100          105          110
E--> 212 ttt cag ggt tca cat gtt ccg tac acg ttc gga ggg ggg acc aag
      213 ctg          384
      214 Phe Gln Gly Ser His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys
W--> 215 Leu
W--> 216          115          120          125
E--> 218 gaa          ata          aaa
      219 393
      220 Glu Ile Lys
W--> 221          130
      224 <210> SEQ ID NO: 4
      225 <211> LENGTH: 131
      226 <212> TYPE: PRT
      227 <213> ORGANISM: Mus musculus
      229 <220> FEATURE:
      230 <221> NAME/KEY: SIGNAL
      231 <222> LOCATION: (1)..(19)
      233 <400> SEQUENCE: 4
      234 Met Lys Leu Pro Val Arg Leu Leu Val Leu Met Phe Trp Ile Pro
E--> 235 Ala
E--> 236 1          5          10          15
      238 Ser Arg Ser Asp Val Leu Met Thr Gln Thr Pro Leu Ser Leu Pro
E--> 239 Val
E--> 240          20          25          30
      242 Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser
E--> 243 Leu
E--> 244          35          40          45
      246 Val His Ser Asn Gly Arg Thr Tyr Leu Glu Trp Tyr Leu Gln Lys

```

*same**same*

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Output Set: N:\CRF4\07082004\J500207.raw

```

E--> 247 Pro
E--> 248      50      55      60
      250 Gly Gln Ser Pro Lys Val Leu Ile Tyr Lys Val Ser Asn Arg Ile
E--> 251 Ser
E--> 252      65      70      75
E--> 253 80
      255 Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe
E--> 256 Thr
E--> 257      85      90      95
      259 Leu Lys Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe
E--> 260 Cys
E--> 261      100      105      110
      263 Phe Gln Gly Ser His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys
E--> 264 Leu
E--> 265      115      120      125
      267 Glu Ile Lys
E--> 268      130
      271 <210> SEQ ID NO: 5
      272 <211> LENGTH: 121
      273 <212> TYPE: PRT
      274 <213> ORGANISM: Mus musculus
      276 <400> SEQUENCE: 5
      277 Gln Val Gln Leu Gln Gln Ser Gly Ala Glu Val Ala Arg Pro Gly
E--> 278 Ala
E--> 279      1      5      10      15
      282 Ser Val Lys Leu Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp
E--> 283 Tyr
E--> 284      20      25      30
      287 Tyr Leu Asn Trp Val Lys Gln Arg Ser Gly Gln Gly Leu Glu Trp
E--> 288 Ile
E--> 289      35      40      45
      292 Gly Glu Ile Asp Pro Gly Ser Asp Ser Ile Tyr Tyr Asn Glu Asn
E--> 293 Leu
E--> 294      50      55      60
      297 Glu Gly Arg Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala
E--> 298 Tyr
E--> 299      65      70      75
E--> 300 80
      303 Met Gln Leu Asn Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe
E--> 304 Cys
E--> 305      85      90      95
      308 Ala Arg Tyr Gly Tyr Ser Arg Tyr Asp Val Arg Phe Val Tyr Trp
E--> 309 Gly
E--> 310      100      105      110
      313 Gln Gly Thr Leu Val Thr Val Ser Thr
E--> 314      115      120
      317 <210> SEQ ID NO: 6
      318 <211> LENGTH: 112
      319 <212> TYPE: PRT

```

*same**same*

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Input Set : A:\Seq. Listing.asc

Output Set: N:\CRF4\07082004\J500207.raw

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320 <213> ORGANISM: Mus musculus
322 <400> SEQUENCE: 6
323 Asp Val Leu Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu
E--> 324 Gly
E--> 325      1              5              10
E--> 326 15
329 Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His
E--> 330 Ser
E--> 331      20              25              30
334 Asn Gly Arg Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro Gly Gln
E--> 335 Ser
E--> 336      35              40              45
339 Pro Lys Val Leu Ile Tyr Lys Val Ser Asn Arg Ile Ser Gly Val
E--> 340 Pro
E--> 341      50              55              60
344 Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys
E--> 345 Ile
E--> 346 65              70              75
E--> 347 80
350 Ser Arg Val Glu Ala Glu Asp Leu Gly Val Tyr Phe Cys Phe Gln
E--> 351 Gly
E--> 352      85              90              95
355 Ser His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile
E--> 356 Lys
E--> 357      100             105             110
370 <210> SEQ ID NO: 8
371 <211> LENGTH: 17
372 <212> TYPE: PRT
373 <213> ORGANISM: Mus musculus
375 <400> SEQUENCE: 8
376 Glu Ile Asp Pro Gly Ser Asp Ser Ile Tyr Tyr Asn Glu Asn Leu
E--> 377 Glu
E--> 378 1              5              10              15
381 Gly
394 <210> SEQ ID NO: 10
395 <211> LENGTH: 16
396 <212> TYPE: PRT
397 <213> ORGANISM: Mus musculus
399 <400> SEQUENCE: 10
400 Arg Ser Ser Gln Ser Leu Val His Ser Asn Gly Arg Thr Tyr Leu
E--> 401 Glu
E--> 402 1              5              10              15
425 <210> SEQ ID NO: 13
426 <211> LENGTH: 22
427 <212> TYPE: DNA
428 <213> ORGANISM: Artificial
430 <220> FEATURE:
431 <223> OTHER INFORMATION: a primer for amplification of KM1334 VH
433 <400> SEQUENCE: 13

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RAW SEQUENCE LISTING

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Input Set : A:\Seq. Listing.asc

Output Set: N:\CRF4\07082004\J500207.raw

E--> 434 ctgaattcgc ↑ ggccgctagt ↑ cc *same*
 435 22
 438 <210> SEQ ID NO: 14
 439 <211> LENGTH: 39
 440 <212> TYPE: DNA
 441 <213> ORGANISM: Artificial
 443 <220> FEATURE:
 444 <223> OTHER INFORMATION: a primer for amplification of KM1334 VH
 446 <400> SEQUENCE: 14

E--> 447 atgggccctt ggtggaggct gtagagacag tgaccagag *same*
 448 39
 451 <210> SEQ ID NO: 15
 452 <211> LENGTH: 22
 453 <212> TYPE: DNA
 454 <213> ORGANISM: Artificial
 456 <220> FEATURE:
 457 <223> OTHER INFORMATION: a primer for amplification of KM1334 VL
 459 <400> SEQUENCE: 15

E--> 460 ctgaattcgc ggccgctgct gt *same*
 461 22
 464 <210> SEQ ID NO: 16
 465 <211> LENGTH: 28
 466 <212> TYPE: DNA
 467 <213> ORGANISM: Artificial
 469 <220> FEATURE:
 470 <223> OTHER INFORMATION: a primer for amplification of KM1334 VL
 472 <400> SEQUENCE: 16

E--> 473 atcgtacgtt ttattttccag cttggtcc *same*
 474 28
 477 <210> SEQ ID NO: 17
 478 <211> LENGTH: 25
 479 <212> TYPE: PRT
 480 <213> ORGANISM: Artificial
 482 <220> FEATURE:
 483 <223> OTHER INFORMATION: human FGF-8 peptide (amino acid residues 23-46)
 484 added ~~an~~ a
 485 cysteine cysteine residue at its C-terminus
 487 <400> SEQUENCE: 17
 488 Gln Val Thr Val Gln Ser Ser Pro Asn Phe Thr Gln His Val Arg *same*

E--> 489 Glu
 E--> 490 1 5 10 15
 493 Gln Ser Leu Val Thr Asp Gln Leu Cys
 E--> 494 20 25
 497 <210> SEQ ID NO: 18
 498 <211> LENGTH: 121
 499 <212> TYPE: PRT
 500 <213> ORGANISM: Artificial
 502 <220> FEATURE:
 503 <223> OTHER INFORMATION: HV.0, a designed amino acid sequence of VH of

do not use TAB codes. They cause processing errors

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TIME: 16:15:05

Input Set : A:\Seq. Listing.asc

Output Set: N:\CRF4\07082004\J500207.raw

504 an anti-FGF-8 CDR-grafted neutralizing antibody
 506 <400> SEQUENCE: 18
 507 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly
 E--> 508 Ala
 E--> 509 1 5 10 15
 512 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp
 E--> 513 Tyr
 E--> 514 20 25 30
 517 Tyr Leu Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp
 E--> 518 Met
 E--> 519 35 40 45
 522 Gly Glu Ile Asp Pro Gly Ser Asp Ser Ile Tyr Tyr Asn Glu Asn
 E--> 523 Leu
 E--> 524 50 55 60
 527 Glu Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Ser Thr Ala
 E--> 528 Tyr
 E--> 529 65 70 75
 E--> 530 80
 533 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr
 E--> 534 Cys
 E--> 535 85 90 95
 537 Ala Arg Tyr Gly Tyr Ser Arg Tyr Asp Val Arg Phe Val Tyr Trp
 E--> 538 Gly
 E--> 539 100 105 110
 542 Gln Gly Thr Leu Val Thr Val Ser Ser
 E--> 543 115 120
 546 <210> SEQ ID NO: 19
 547 <211> LENGTH: 112
 548 <212> TYPE: PRT
 549 <213> ORGANISM: Artificial
 551 <220> FEATURE:
 552 <223> OTHER INFORMATION: LV.0, a designed amino acid sequence of VL of
 553 an anti-FGF-8 CDR-grafted neutralizing antibody
 555 <400> SEQUENCE: 19
 556 Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro
 E--> 557 Gly
 E--> 558 1 5 10 15
 561 Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His
 E--> 562 Ser
 E--> 563 20 25 30
 566 Asn Gly Arg Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro Gly Gln
 E--> 567 Ser
 E--> 568 35 40 45
 571 Pro Gln Leu Leu Ile Tyr Lys Val Ser Asn Arg Ile Ser Gly Val
 E--> 572 Pro
 E--> 573 50 55 60
 576 Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys
 E--> 577 Ile
 E--> 578 65 70 75

*same**same*

RAW SEQUENCE LISTING

DATE: 07/08/2004

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TIME: 16:15:05

Input Set : A:\Seq. Listing.asc

Output Set : N:\CRF4\07082004\J500207.raw

```

E--> 579 80
      582 Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Phe Gln
E--> 583 Gly
E--> 584                85                90                95
      587 Ser His Val Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
E--> 588 Lys
E--> 589                100                105                110
      592 <210> SEQ ID NO: 20
      593 <211> LENGTH: 121
      594 <212> TYPE: PRT
      595 <213> ORGANISM: Artificial
      597 <220> FEATURE:
      598 <223> OTHER INFORMATION: HV.6, a designed amino acid sequence of VH of
      599       an anti-FGF-8 CDR-grafted neutralizing antibody
      601 <400> SEQUENCE: 20
      602 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Ala Arg Pro Gly
E--> 603 Ala
E--> 604      1                5                10                15
      607 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp
E--> 608 Tyr
E--> 609                20                25                30
      612 Tyr Leu Asn Trp Val Arg Gln Arg Ser Gly Gln Gly Leu Glu Trp
E--> 613 Ile
E--> 614                35                40                45
      617 Gly Glu Ile Asp Pro Gly Ser Asp Ser Ile Tyr Tyr Asn Glu Asn
E--> 618 Leu
E--> 619                50                55                60
      622 Glu Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Ser Thr Ala
E--> 623 Tyr
E--> 624                65                70                75
E--> 625 80
      628 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Phe
E--> 629 Cys
E--> 630                85                90                95
      633 Ala Arg Tyr Gly Tyr Ser Arg Tyr Asp Val Arg Phe Val Tyr Trp
E--> 634 Gly
E--> 635                100                105                110
      638 Gln Gly Thr Leu Val Thr Val Ser Ser
E--> 639                115                120
      642 <210> SEQ ID NO: 21
      643 <211> LENGTH: 112
      644 <212> TYPE: PRT
      645 <213> ORGANISM: Artificial
      647 <220> FEATURE:
      648 <223> OTHER INFORMATION: LV.6, a designed amino acid sequence of VL of
      649       an anti-FGF-8 CDR-grafted neutralizing antibody
      651 <400> SEQUENCE: 21
      652 Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Ser Leu
E--> 653 Gly

```

*same**same*

RAW SEQUENCE LISTING

DATE: 07/08/2004

PATENT APPLICATION: US/10/500,207

TIME: 16:15:05

Input Set : A:\Seq. Listing.asc

Output Set : N:\CRF4\07082004\J500207.raw

```

E--> 654   1           5           10           15
      657 Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His
E--> 658 Ser
E--> 659           20           25           30
      662 Asn Gly Arg Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro Gly Gln
E--> 663 Ser
E--> 664           35           40           45
      667 Pro Lys Val Leu Ile Tyr Lys Val Ser Asn Arg Ile Ser Gly Val
E--> 668 Pro
E--> 669           50           55           60
      672 Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys
E--> 673 Ile
E--> 674           65           70           75
E--> 675 80
      678 Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Phe Cys Phe Gln
E--> 679 Gly
E--> 680           85           90           95
      683 Ser His Val Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
E--> 684 Lys
E--> 685           100          105          110
      688 <210> SEQ ID NO: 22
      689 <211> LENGTH: 504
      690 <212> TYPE: DNA
      691 <213> ORGANISM: Artificial
      693 <220> FEATURE:
      694 <223> OTHER INFORMATION: a DNA encoding HV.0
      696 <220> FEATURE:
      697 <221> NAME/KEY: CDS
      698 <222> LOCATION: (47)..(466)
      700 <220> FEATURE:
      701 <221> NAME/KEY: sig_peptide
      702 <222> LOCATION: (47)..(103)
      704 <400> SEQUENCE: 22
E--> 705 caggaaacag ctatgacgaa ttcgcggccg cacactgact ctaacc atg gaa
      706 tgg           55
      707                               Met Glu
W--> 708 Trp
E--> 711 atc tgg atc ttt ctc ttc ttc ctc tca gga act aca ggt gtc tac
      712 tcc           103
      713 Ile Trp Ile Phe Leu Phe Phe Leu Ser Gly Thr Thr Gly Val Tyr
W--> 714 Ser
W--> 715          -15          -10          -5
E--> 716 -1
E--> 718 cag gtg cag ctg gtg cag tct ggg gct gag gtg aag aag ccc ggg
      719 gcc           151
      720 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys Pro Gly
W--> 721 Ala
W--> 722   1           5           10           15
E--> 724 tca gtg aag gtc tcc tgc aag gct tct gga tac acc ttc act gac

```

*same**same*

RAW SEQUENCE LISTING

DATE: 07/08/2004

PATENT APPLICATION: US/10/500,207

TIME: 16:15:05

Input Set : A:\Seq. Listing.asc

Output Set: N:\CRF4\07082004\J500207.raw

```

725 tac      199
726 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp
W--> 727 Tyr
W--> 728      20      25      30
E--> 730 tat cta aac tgg gtg cgg cag gcc ccc gga caa ggg ctt gag tgg
731 atg      247
732 Tyr Leu Asn Trp Val Arg Gln Ala Pro Gly Gln Gly Leu Glu Trp
W--> 733 Met
W--> 734      35      40      45
E--> 736 gga gag atc gat cct gga agt gat agt ata tat tat aat gaa aac
737 ttg      295
738 Gly Glu Ile Asp Pro Gly Ser Asp Ser Ile Tyr Tyr Asn Glu Asn
W--> 739 Leu
W--> 740      50      55      60
E--> 742 gag ggc aga gtc acg att acc gcg gac aca tcc acg agc aca gcc
743 tac      343
744 Glu Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Ser Thr Ala
W--> 745 Tyr
W--> 746      65      70      75
E--> 747 80
E--> 749 atg gag ctg agc agc ctg aga tct gag gac acg gcc gtg tat tac
750 tgt      391
751 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Tyr
W--> 752 Cys
W--> 753      85      90      95
E--> 755 gcg aga tat ggg tat tct aga tac gac gta agg ttt gtc tac tgg
756 ggc      439
757 Ala Arg Tyr Gly Tyr Ser Arg Tyr Asp Val Arg Phe Val Tyr Trp
W--> 758 Gly
W--> 759      100      105      110
E--> 761 cag gga acc ctg gtc acc gtc tcc tca gcctccacca agggcccact
762 486
763 Gln Gly Thr Leu Val Thr Val Ser Ser
W--> 764      115      120
E--> 766 agtcgtgact gggaaaac
767 504
770 <210> SEQ ID NO: 23
771 <211> LENGTH: 141
772 <212> TYPE: DNA
773 <213> ORGANISM: Artificial
775 <220> FEATURE:
776 <223> OTHER INFORMATION: a synthetic DNA for construction of a DNA encoding
777 HV.0
779 <400> SEQUENCE: 23
E--> 780 caggaaacag ctatgacgaa ttgcgggccg cacactgact ctaaccatgg
781 aatggatctg 60
E--> 783 gatctttctc ttcttctctc caggaactac aggtgtctac tcccaggtgc
784 agctgggtgca 120
E--> 786 gtctggggct gaggtgaaga a

```

same

no TAB
codes
do NOT use
TAB codes

same

RAW SEQUENCE LISTING

DATE: 07/08/2004

PATENT APPLICATION: US/10/500,207

TIME: 16:15:05

Input Set : A:\Seq. Listing.asc

Output Set: N:\CRF4\07082004\J500207.raw

```

787 141
790 <210> SEQ ID NO: 24
791 <211> LENGTH: 141
792 <212> TYPE: DNA
793 <213> ORGANISM: Artificial
795 <220> FEATURE:
796 <223> OTHER INFORMATION: a synthetic DNA for construction of a DNA encoding
797     HV.0
799 <400> SEQUENCE: 24
E--> 800 aggatcgatc   tctcccatcc   actcaagccc   ttgtccgggg   gcctgccgca
801   ccaggtttag       60
E--> 803 atagtagtca   gtgaaggtgt   atccagaagc   cttgcaggag   accttcactg
804   aggccccggg       120
E--> 806 cttcttcacc           tcagccccag           a
807 141
810 <210> SEQ ID NO: 25
811 <211> LENGTH: 141
812 <212> TYPE: DNA
813 <213> ORGANISM: Artificial
815 <220> FEATURE:
816 <223> OTHER INFORMATION: a synthetic DNA for construction of a DNA encoding
817     HV.0
819 <400> SEQUENCE: 25
E--> 820 ggatggggaga   gatcgatcct   ggaagtgata   gtatatatta   taatgaaaac
821   ttggaggggca       60
E--> 823 gagtcacgat   taccgcggac   acatccacga   gcacagccta   catggagctg
824   agcagcctga       120
E--> 826 gatctgagga           cacggccgtg           t
827 141
830 <210> SEQ ID NO: 26
831 <211> LENGTH: 141
832 <212> TYPE: DNA
833 <213> ORGANISM: Artificial
835 <220> FEATURE:
836 <223> OTHER INFORMATION: a synthetic DNA for construction of a DNA encoding
837     HV.0
839 <400> SEQUENCE: 26
E--> 840 gttttcccag   tcacgactag   tgggcccttg   gtggaggctg   aggagacggt
841   gaccaggggt       60
E--> 843 ccctggcccc   agtagacaaa   ccttacgtcg   tatctagaat   acccatatct
844   cgcacagtaa       120
E--> 846 tacacggccg           tgtcctcaga           t
847 141
850 <210> SEQ ID NO: 27
851 <211> LENGTH: 504
852 <212> TYPE: DNA
853 <213> ORGANISM: Artificial
855 <220> FEATURE:
856 <223> OTHER INFORMATION: a DNA encoding HV.6

```

*same**same**same*

RAW SEQUENCE LISTING

DATE: 07/08/2004

PATENT APPLICATION: US/10/500,207

TIME: 16:15:05

Input Set : A:\Seq. Listing.asc

Output Set: N:\CRF4\07082004\J500207.raw

```

858 <220> FEATURE:
859 <221> NAME/KEY: CDS
860 <222> LOCATION: (47)..(466)
862 <220> FEATURE:
863 <221> NAME/KEY: sig_peptide
864 <222> LOCATION: (47)..(103)
866 <400> SEQUENCE: 27
E--> 867 caggaaacag ctatgacgaa ttcgcggcccg cacactgact ctaacc atg gaa
868 tgg 55
869 Met Glu
W--> 870 Trp
E--> 873 atc tgg atc ttt ctc ttc ttc ttc tca gga act aca ggt gtc tac
874 tcc 103
875 Ile Trp Ile Phe Leu Phe Phe Leu Ser Gly Thr Thr Gly Val Tyr
W--> 876 Ser
E--> 877 -15 -10 -5
E--> 878 -1
E--> 880 cag gtg cag ctg gtg cag tct ggg gct gag gtg gcg agg ccc ggg
881 gcc 151
882 Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Ala Arg Pro Gly
W--> 883 Ala
E--> 884 1 5 10 15
E--> 886 tca gtg aag gtc tcc tgc aag gct tct gga tac acc ttc act gac
887 tac 199
888 Ser Val Lys Val Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp
W--> 889 Tyr
E--> 890 20 25 30
E--> 892 tat cta aac tgg gtg cgg cag agg tct gga caa ggg ctt gag tgg
893 att 247
894 Tyr Leu Asn Trp Val Arg Gln Arg Ser Gly Gln Gly Leu Glu Trp
W--> 895 Ile
E--> 896 35 40 45
E--> 898 gga gag atc gat cct gga agt gat agt ata tat tat aat gaa aac
899 ttg 295
900 Gly Glu Ile Asp Pro Gly Ser Asp Ser Ile Tyr Tyr Asn Glu Asn
W--> 901 Leu
E--> 902 50 55 60
E--> 904 gag ggc aga gtc acg att acc gcg gac aca tcc acg agc aca gcc
905 tac 343
906 Glu Gly Arg Val Thr Ile Thr Ala Asp Thr Ser Thr Ser Thr Ala
W--> 907 Tyr
E--> 908 65 70 75
E--> 909 80
E--> 911 atg gag ctg agc agc ctg aga tct gag gac acg gcc gtg tat ttc
912 tgt 391
913 Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr Phe
W--> 914 Cys
E--> 915 85 90 95
E--> 917 gcg aga tat ggg tat tct aga tac gac gta agg ttt gtc tac tgg

```

same

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/500,207

DATE: 07/08/2004

TIME: 16:15:05

Input Set : A:\Seq. Listing.asc

Output Set: N:\CRF4\07082004\J500207.raw

```

918 ggc          439
919 Ala Arg Tyr Gly Tyr Ser Arg Tyr Asp Val Arg Phe Val Tyr Trp
W--> 920 Gly
W--> 921          100          105          110
E--> 923 cag gga acc ctg gtc acc gtc tcc tca gcctccacca agggcccact
924 486
925 Gln Gly Thr Leu Val Thr Val Ser Ser
W--> 926          115          120
E--> 928 agtcgtgact gggaaaaac
929 504
932 <210> SEQ ID NO: 28
933 <211> LENGTH: 141
934 <212> TYPE: DNA
935 <213> ORGANISM: Artificial
937 <220> FEATURE:
938 <223> OTHER INFORMATION: a synthetic DNA for construction of a DNA encoding
939 HV.6
941 <400> SEQUENCE: 28
E--> 942 caggaaacag ctatgacgaa ttcgcggccg cacactgact ctaaccatgg
943 aatggatctg 60
E--> 945 gatctttctc ttcttctctc caggaactac aggtgtctac tcccaggtgc
946 agctggtgca 120
E--> 948 gtctggggct gaggtggcga g
949 141
952 <210> SEQ ID NO: 29
953 <211> LENGTH: 141
954 <212> TYPE: DNA
955 <213> ORGANISM: Artificial
957 <220> FEATURE:
958 <223> OTHER INFORMATION: a synthetic DNA for construction of a DNA encoding
959 HV.6
961 <400> SEQUENCE: 29
E--> 962 aggatcgatc tctccaatcc actcaagccc ttgtccagac ctctgccgca
963 cccagtttag 60
E--> 965 atagtagtca gtgaaggtgt atccagaagc cttgcaggag accttcactg
966 aggccccggg 120
E--> 968 cctcgccacc tcagccccag a
969 141
972 <210> SEQ ID NO: 30
973 <211> LENGTH: 141
974 <212> TYPE: DNA
975 <213> ORGANISM: Artificial
977 <220> FEATURE:
978 <223> OTHER INFORMATION: a synthetic DNA for construction of a DNA encoding
979 HV.6
981 <400> SEQUENCE: 30
E--> 982 ggattggaga gatcgatcct ggaagtgata gtatatatta taatgaaaac
983 ttggagggca 60
E--> 985 gagtcacgat taccgcgga acatccacga gcacagccta catggagctg

```

same

same

same

same

RAW SEQUENCE LISTING

DATE: 07/08/2004

PATENT APPLICATION: US/10/500,207

TIME: 16:15:05

Input Set : A:\Seq. Listing.asc

Output Set: N:\CRF4\07082004\J500207.raw

```

986 agcagcctga      120
E--> 988 gatctgagga      cacggccgtg      t
989 141
992 <210> SEQ ID NO: 31
993 <211> LENGTH: 141
994 <212> TYPE: DNA
995 <213> ORGANISM: Artificial
997 <220> FEATURE:
998 <223> OTHER INFORMATION: a synthetic DNA for construction of a DNA encoding
999      HV.6
1001 <400> SEQUENCE: 31
E--> 1002 gttttccag      tcacgactag      tgggcccttg      gtggaggctg      aggagacggt
1003 gaccagggtt      60
E--> 1005 ccctggcccc      agtagacaaa      ccttacgtcg      tatctagaat      acccatatct
1006 cgcacagaaa      120
E--> 1008 tacacggccg      tgtcctcaga      t
1009 141
1012 <210> SEQ ID NO: 32
1013 <211> LENGTH: 459
1014 <212> TYPE: DNA
1015 <213> ORGANISM: Artificial
1017 <220> FEATURE:
1018 <223> OTHER INFORMATION: a DNA encoding LV.0
1020 <220> FEATURE:
1021 <221> NAME/KEY: CDS
1022 <222> LOCATION: (40)..(432)
1024 <220> FEATURE:
1025 <221> NAME/KEY: sig_peptide
1026 <222> LOCATION: (40)..(96)
1028 <400> SEQUENCE: 32
E--> 1030 caggaaacag      ctatgacgaa      ttcaggttgc      ctctcaaa      atg      aag      ttg      cct
1031 gtt      54
1032      Met Lys Leu Pro
W--> 1033 Val
1035 -15
E--> 1037 agg      ctg      ttg      gtg      ctg      atg      ttc      tgg      att      cct      gct      tcc      agg      agt      gat
1038 atc      102
1039 Arg Leu Leu Val Leu Met Phe Trp Ile Pro Ala Ser Arg Ser Asp
W--> 1040 Ile
W--> 1041      -10      -5      -1      1
E--> 1043 gtg      atg      act      cag      tct      cca      ctc      tcc      ctg      ccc      gtc      acc      cct      gga      gag
1044 ccg      150
1045 Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly Glu
W--> 1046 Pro
W--> 1047      5      10      15
E--> 1049 gcc      tcc      atc      tcc      tgc      aga      tct      agt      cag      agt      ctt      gta      cat      agt      aat
1050 gga      198
1051 Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His Ser Asn
W--> 1052 Gly

```

RAW SEQUENCE LISTING

DATE: 07/08/2004

PATENT APPLICATION: US/10/500,207

TIME: 16:15:05

Input Set : A:\Seq. Listing.asc

Output Set: N:\CRF4\07082004\J500207.raw

```

W--> 1053      20              25              30
E--> 1055 aga acc tat tta gaa tgg tac ctg cag aag cca ggc cag tct cca
      1056 cag      246
      1057 Arg Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro
W--> 1058 Gln
W--> 1059      35              40              45
E--> 1060 50
E--> 1062 ctc ctg atc tat aaa gtt tcc aac cga att tct ggg gtc cca gac
      1063 agg      294
      1064 Leu Leu Ile Tyr Lys Val Ser Asn Arg Ile Ser Gly Val Pro Asp
W--> 1065 Arg
W--> 1066      55              60              65
E--> 1068 ttc agt ggc agt gga tcc ggg aca gat ttc aca ctg aaa atc agc
      1069 agg      342
      1070 Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser
W--> 1071 Arg
W--> 1072      70              75              80
E--> 1074 gtg gag gct gag gac gtc ggg gtt tat tac tgc ttt cag ggt tca
      1075 cat      390
      1076 Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Phe Gln Gly Ser
W--> 1077 His
W--> 1078      85              90              95
E--> 1080 gtt ccg tac acg ttc ggc caa ggg acc aag gtg gaa atc aaa
      1081 432
      1082 Val Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
W--> 1083      100              105              110
E--> 1085 cgtacgacta      gtcgtgactg      ggaaaac
      1086 459
      1089 <210> SEQ ID NO: 33
      1090 <211> LENGTH: 130
      1091 <212> TYPE: DNA
      1092 <213> ORGANISM: Artificial
      1094 <220> FEATURE:
      1095 <223> OTHER INFORMATION: a synthetic DNA for construction of a DNA encoding
      1096 LV.0
      1098 <400> SEQUENCE: 33
E--> 1099 caggaaacag ctatgacgaa ttcaggttgc ctctcaaaa tgaagttgcc
      1100 tgtaggctg      60
E--> 1102 ttggtgctga tggtctggat tcttcttcc aggagtgata tcgtgatgac
      1103 tcagtctcca      120
E--> 1105 ctctccctgc
      1106 130
      1109 <210> SEQ ID NO: 34
      1110 <211> LENGTH: 130
      1111 <212> TYPE: DNA
      1112 <213> ORGANISM: Artificial
      1114 <220> FEATURE:
      1115 <223> OTHER INFORMATION: a synthetic DNA for construction of a DNA encoding
      1116 LV.0

```

RAW SEQUENCE LISTING

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TIME: 16:15:05

Input Set : A:\Seq. Listing.asc

Output Set: N:\CRF4\07082004\J500207.raw

```

1118 <400> SEQUENCE: 34
E--> 1119 agactggcct    ggcttctgca    ggtaccattc    taaataggtt    cttccattac
1120 tatgtacaag        60
E--> 1122 actctgacta    gatctgcagg    agatggaggc    cggtctcca    ggggtgacgg
1123 gcagggagag        120
E--> 1125 tggagactga
1126 130
1129 <210> SEQ ID NO: 35
1130 <211> LENGTH: 130
1131 <212> TYPE: DNA
1132 <213> ORGANISM: Artificial
1134 <220> FEATURE:
1135 <223> OTHER INFORMATION: a synthetic DNA for construction of a DNA encoding
1136 LV.0
1138 <400> SEQUENCE: 35
E--> 1139 tgcagaagcc    aggccagtct    ccacagctcc    tgatctataa    agtttccaac
1140 cgaatttctg        60
E--> 1142 ggggtcccaga    caggttcagt    ggcagtggat    ccgggacaga    tttcacactg
1143 aaaatcagca        120
E--> 1145 ggggtggaggc
1146 130
1327 <210> SEQ ID NO: 42
1328 <211> LENGTH: 112
1329 <212> TYPE: PRT
1330 <213> ORGANISM: Artificial
1332 <220> FEATURE:
1333 <223> OTHER INFORMATION: LV.4-1, a designed amino acid sequence of VL of
1334 an anti-FGF-8 CDR-grafted neutralizing antibody
1336 <400> SEQUENCE: 42
1337 Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro
E--> 1338 Gly
E--> 1339 1          5          10          15
1342 Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His
E--> 1343 Ser
E--> 1344 20          25          30
1347 Asn Gly Arg Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro Gly Gln
E--> 1348 Ser
E--> 1349 35          40          45
1352 Pro Lys Val Leu Ile Tyr Lys Val Ser Asn Arg Ile Ser Gly Val
E--> 1353 Pro
E--> 1354 50          55          60
1357 Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys
E--> 1358 Ile
E--> 1359 65          70          75
E--> 1360 80
1363 Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Phe Cys Phe Gln
E--> 1364 Gly
E--> 1365 85          90          95
1368 Ser His Val Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile

```

RAW SEQUENCE LISTING

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TIME: 16:15:05

Input Set : A:\Seq. Listing.asc

Output Set: N:\CRF4\07082004\J500207.raw

```

E--> 1369 Lys
E--> 1370      100      105      110
1373 <210> SEQ ID NO: 43
1374 <211> LENGTH: 112
1375 <212> TYPE: PRT
1376 <213> ORGANISM: Artificial Sequence
1378 <220> FEATURE:
1379 <223> OTHER INFORMATION: LV.4-2, a designed amino acid sequence of VL of
1380      an anti-FGF-8 CDR-grafted neutralizing antibody
1382 <400> SEQUENCE: 43
1383 Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Ser Leu
E--> 1384 Gly
E--> 1385      1      5      10      15
1388 Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His
E--> 1389 Ser
E--> 1390      20      25      30
1393 Asn Gly Arg Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro Gly Gln
E--> 1394 Ser
E--> 1395      35      40      45
1398 Pro Gln Leu Leu Ile Tyr Lys Val Ser Asn Arg Ile Ser Gly Val
E--> 1399 Pro
E--> 1400      50      55      60
1403 Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys
E--> 1404 Ile
E--> 1405      65      70      75
E--> 1406 80
1409 Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Phe Cys Phe Gln
E--> 1410 Gly
E--> 1411      85      90      95
1414 Ser His Val Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
E--> 1415 Lys
E--> 1416      100      105      110
1419 <210> SEQ ID NO: 44
1420 <211> LENGTH: 112
1421 <212> TYPE: PRT
1422 <213> ORGANISM: Artificial
1424 <220> FEATURE:
1425 <223> OTHER INFORMATION: LV.3-1, a designed amino acid sequence of VL of
1426      an anti-FGF-8 CDR-grafted neutralizing antibody
1428 <400> SEQUENCE: 44
1429 Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro
E--> 1430 Gly
E--> 1431      1      5      10      15
1434 Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His
E--> 1435 Ser
E--> 1436      20      25      30
1439 Asn Gly Arg Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro Gly Gln
E--> 1440 Ser
E--> 1441      35      40      45

```

RAW SEQUENCE LISTING

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TIME: 16:15:05

Input Set : A:\Seq. Listing.asc

Output Set: N:\CRF4\07082004\J500207.raw

```

1444 Pro Gln Val Leu Ile Tyr Lys Val Ser Asn Arg Ile Ser Gly Val
E--> 1445 Pro
E--> 1446      50                      55                      60
1449 Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys
E--> 1450 Ile
E--> 1451      65                      70                      75
E--> 1452 80
1455 Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Phe Cys Phe Gln
E--> 1456 Gly
E--> 1457      85                      90                      95
1460 Ser His Val Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
E--> 1461 Lys
E--> 1462      100                    105                    110
1465 <210> SEQ ID NO: 45
1466 <211> LENGTH: 112
1467 <212> TYPE: PRT
1468 <213> ORGANISM: Artificial
1470 <220> FEATURE:
1471 <223> OTHER INFORMATION: LV.3-2, a designed amino acid sequence of VL of
1472      an anti-FGF-8 CDR-grafted neutralizing antibody
1474 <400> SEQUENCE: 45
1475 Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Ser Leu
E--> 1476 Gly
E--> 1477      1                      5                      10                      15
1480 Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His
E--> 1481 Ser
E--> 1482      20                      25                      30
1485 Asn Gly Arg Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro Gly Gln
E--> 1486 Ser
E--> 1487      35                      40                      45
1490 Pro Gln Leu Leu Ile Tyr Lys Val Ser Asn Arg Ile Ser Gly Val
E--> 1491 Pro
E--> 1492      50                      55                      60
1495 Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys
E--> 1496 Ile
E--> 1497      65                      70                      75
E--> 1498 80
1501 Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Phe Cys Phe Gln
E--> 1502 Gly
E--> 1503      85                      90                      95
1506 Ser His Val Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
E--> 1507 Lys
E--> 1508      100                    105                    110
1511 <210> SEQ ID NO: 46
1512 <211> LENGTH: 112
1513 <212> TYPE: PRT
1514 <213> ORGANISM: Artificial
1516 <220> FEATURE:
1517 <223> OTHER INFORMATION: LV.2-1, a designed amino acid sequence of VL of

```

same

RAW SEQUENCE LISTING

DATE: 07/08/2004

PATENT APPLICATION: US/10/500,207

TIME: 16:15:05

Input Set : A:\Seq. Listing.asc

Output Set: N:\CRF4\07082004\J500207.raw

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1518      an anti-FGF-8 CDR-grafted neutralizing antibody
1520 <400> SEQUENCE: 46
1521 Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro
E--> 1522 Gly
E--> 1523      1              5              10              15
1526 Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His
E--> 1527 Ser
E--> 1528      20              25              30
1531 Asn Gly Arg Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro Gly Gln
E--> 1532 Ser
E--> 1533      35              40              45
1536 Pro Gln Val Leu Ile Tyr Lys Val Ser Asn Arg Ile Ser Gly Val
E--> 1537 Pro
E--> 1538      50              55              60
1541 Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys
E--> 1542 Ile
E--> 1543      65              70              75
E--> 1544 80
1547 Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Phe Cys Phe Gln
E--> 1548 Gly
E--> 1549      85              90              95
1552 Ser His Val Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
E--> 1553 Lys
E--> 1554      100             105             110
1557 <210> SEQ ID NO: 47
1558 <211> LENGTH: 112
1559 <212> TYPE: PRT
1560 <213> ORGANISM: Artificial
1562 <220> FEATURE:
1563 <223> OTHER INFORMATION: LV.2-2, a designed amino acid sequence of VL of
1564      an anti-FGF-8 CDR-grafted neutralizing antibody
1566 <400> SEQUENCE: 47
1567 Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro
E--> 1568 Gly
E--> 1569      1              5              10              15
1572 Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His
E--> 1573 Ser
E--> 1574      20              25              30
1577 Asn Gly Arg Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro Gly Gln
E--> 1578 Ser
E--> 1579      35              40              45
1582 Pro Gln Leu Leu Ile Tyr Lys Val Ser Asn Arg Ile Ser Gly Val
E--> 1583 Pro
E--> 1584      50              55              60
1587 Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys
E--> 1588 Ile
E--> 1589      65              70              75
E--> 1590 80
1593 Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Phe Cys Phe Gln

```

same

same

RAW SEQUENCE LISTING

DATE: 07/08/2004

PATENT APPLICATION: US/10/500,207

TIME: 16:15:05

Input Set : A:\Seq. Listing.asc

Output Set: N:\CRF4\07082004\J500207.raw

```

E--> 1594 Gly
E--> 1595      85      90      95
      1598 Ser His Val Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
E--> 1599 Lys
E--> 1600      100      105      110
      1629 <210> SEQ ID NO: 50
      1630 <211> LENGTH: 112
      1631 <212> TYPE: PRT
      1632 <213> ORGANISM: Artificial
      1634 <220> FEATURE:
      1635 <223> OTHER INFORMATION: LV.4-3, a designed amino acid sequence of VL of
      1636      an anti-FGF-8 CDR-grafted neutralizing antibody
      1638 <400> SEQUENCE: 50
      1639 Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Ser Leu
E--> 1640 Gly
E--> 1641      1      5      10      15
      1644 Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His
E--> 1645 Ser
E--> 1646      20      25      30
      1649 Asn Gly Arg Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro Gly Gln
E--> 1650 Ser
E--> 1651      35      40      45
      1654 Pro Gln Val Leu Ile Tyr Lys Val Ser Asn Arg Ile Ser Gly Val
E--> 1655 Pro
E--> 1656      50      55      60
      1659 Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys
E--> 1660 Ile
E--> 1661      65      70      75
E--> 1662 80
      1665 Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Phe Cys Phe Gln
E--> 1666 Gly
E--> 1667      85      90      95
      1670 Ser His Val Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
E--> 1671 Lys
E--> 1672      100      105      110
      1675 <210> SEQ ID NO: 51
      1676 <211> LENGTH: 112
      1677 <212> TYPE: PRT
      1678 <213> ORGANISM: Artificial
      1680 <220> FEATURE:
      1681 <223> OTHER INFORMATION: LV.3-3, a designed amino acid sequence of VL of
      1682      an anti-FGF-8 CDR-grafted neutralizing antibody
      1684 <400> SEQUENCE: 51
      1685 Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Ser Leu
E--> 1686 Gly
E--> 1687      1      5      10      15
      1690 Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val His
E--> 1691 Ser
E--> 1692      20      25      30

```

RAW SEQUENCE LISTING

DATE: 07/08/2004

PATENT APPLICATION: US/10/500,207

TIME: 16:15:05

Input Set : A:\Seq. Listing.asc

Output Set: N:\CRF4\07082004\J500207.raw

1695 Asn Gly Arg Thr Tyr Leu Glu Trp Tyr Leu Gln Lys Pro Gly Gln
E--> 1696 Ser
E--> 1697 35 40 45
1700 Pro Gln Val Leu Ile Tyr Lys Val Ser Asn Arg Ile Ser Gly Val
E--> 1701 Pro
E--> 1702 50 55 60
1705 Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys
E--> 1706 Ile
E--> 1707 65 70 75
E--> 1708 80
1711 Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Phe Gln
E--> 1712 Gly
E--> 1713 85 90 95
1716 Ser His Val Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu Ile
E--> 1717 Lys
E--> 1718 100 105 110

same

RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/500,207

DATE: 07/08/2004
TIME: 16:15:06

Input Set : A:\Seq. Listing.asc
Output Set: N:\CRF4\07082004\J500207.raw

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,32,33,34,35,36
Seq#:37,38,39,40,41,42,44,45,46,47,48,49,50,51

VERIFICATION SUMMARY

DATE: 07/08/2004

PATENT APPLICATION: US/10/500,207

TIME: 16:15:06

Input Set : A:\Seq. Listing.asc

Output Set: N:\CRF4\07082004\J500207.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:40 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:45 SEQ:1
L:43 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:44 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
M:254 Repeated in SeqNo=1
L:49 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:50 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:55 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:56 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:61 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:62 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:67 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:68 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:74 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:75 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:80 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:81 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:86 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:87 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:92 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:106 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
M:332 Repeated in SeqNo=2
L:165 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:169 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:45 SEQ:3
L:172 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:173 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
M:254 Repeated in SeqNo=3
L:178 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:179 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:184 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:185 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:190 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:191 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:196 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:197 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:203 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:204 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:209 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:210 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:215 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:216 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:221 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
L:235 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:4
M:332 Repeated in SeqNo=4
L:278 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:5
M:332 Repeated in SeqNo=5
L:324 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:6

VERIFICATION SUMMARY

DATE: 07/08/2004

PATENT APPLICATION: US/10/500,207

TIME: 16:15:06

Input Set : A:\Seq. Listing.asc

Output Set: N:\CRF4\07082004\J500207.raw

M:332 Repeated in SeqNo=6
L:377 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:8
M:332 Repeated in SeqNo=8
L:401 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:10
M:332 Repeated in SeqNo=10
L:434 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:22 SEQ:13
L:447 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:39 SEQ:14
L:460 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:22 SEQ:15
L:473 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:28 SEQ:16
L:489 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:17
M:332 Repeated in SeqNo=17
L:508 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:18
M:332 Repeated in SeqNo=18
L:557 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:19
M:332 Repeated in SeqNo=19
L:603 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:20
M:332 Repeated in SeqNo=20
L:653 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:21
M:332 Repeated in SeqNo=21
L:705 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:52 SEQ:22
L:708 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:22
M:254 Repeated in SeqNo=22
L:714 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:22
L:715 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:22
L:721 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:22
L:722 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:22
L:727 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:22
L:728 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:22
L:733 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:22
L:734 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:22
L:739 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:22
L:740 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:22
L:745 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:22
L:746 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:22
L:752 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:22
L:753 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:22
L:758 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:22
L:780 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:23
M:254 Repeated in SeqNo=23
L:800 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:24
M:254 Repeated in SeqNo=24
L:820 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:25
M:254 Repeated in SeqNo=25
L:840 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:26
M:254 Repeated in SeqNo=26
L:867 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:52 SEQ:27
M:254 Repeated in SeqNo=27
L:942 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:28
M:254 Repeated in SeqNo=28

VERIFICATION SUMMARY

DATE: 07/08/2004

PATENT APPLICATION: US/10/500,207

TIME: 16:15:06

Input Set : A:\Seq. Listing.asc

Output Set: N:\CRF4\07082004\J500207.raw

L:962 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:29
M:254 Repeated in SeqNo=29
L:982 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:30
M:254 Repeated in SeqNo=30
L:1002 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:31
M:254 Repeated in SeqNo=31
L:1030 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:51 SEQ:32
M:254 Repeated in SeqNo=32
L:1099 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:33
M:254 Repeated in SeqNo=33
L:1119 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:34
M:254 Repeated in SeqNo=34
L:1139 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:35
M:254 Repeated in SeqNo=35
L:1159 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:36
M:254 Repeated in SeqNo=36
L:1186 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:51 SEQ:37
M:254 Repeated in SeqNo=37
L:1256 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:38
M:254 Repeated in SeqNo=38
L:1276 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:39
M:254 Repeated in SeqNo=39
L:1297 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:40
M:254 Repeated in SeqNo=40
L:1317 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:41
M:254 Repeated in SeqNo=41
L:1338 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:42
M:332 Repeated in SeqNo=42
L:1384 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:43
M:332 Repeated in SeqNo=43
L:1430 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:44
M:332 Repeated in SeqNo=44
L:1476 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:45
M:332 Repeated in SeqNo=45
L:1522 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:46
M:332 Repeated in SeqNo=46
L:1568 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:47
M:332 Repeated in SeqNo=47
L:1612 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:39 SEQ:48
L:1625 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:39 SEQ:49
L:1640 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:50
M:332 Repeated in SeqNo=50
L:1686 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:51
M:332 Repeated in SeqNo=51